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<110> TOJI, SHINGO
YANO, MINORU
TAMAI, KATSUYUKI

<120> THIOREDOXIN REDUCTASE II

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<140> 09/830,706

<141> 2001-04-27

<150> PCT/JP99/05983

<151> 1999-10-28

<150> JP 1998-310422

<151> 1998-10-30

<160> 38

<170> PatentIn Ver. 2.1

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Arg Thr Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala

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25

30

gca gca ggt cag cgg gac tat gat ctc ctg gtg gtc ggc ggg gga tct 147

Ala Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser

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Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val

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gcc gtg gtg gac tac gtg gaa cct tct ccc caa ggc acc cgg tgg ggc 243

Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly

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ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc ccc aag aag ctg atg	291
Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met	
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cac cag gcg gca ctg ctg gga ggc ctg atc caa gat gcc ccc aac tat	339
His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr	
95 100 105 110	
ggc tgg gag gtg gcc cag ccc gtg ccg cat gac tgg agg aag atg gca	387
Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala	
115 120 125	
gaa gct gtt caa aat cac gtg aaa tcc ttg aac tgg ggc cac cgt gtc	435
Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val	
130 135 140	
cag ctt cag gac aga aaa gtc aag tac ttt aac atc aaa gcc agc ttt	483
Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe	
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Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile	
160 165 170	
ctg ctg tca gcc gat cac atc atc att gct act gga ggg cgg ccg aga	579
Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg	
175 180 185 190	
tac ccc acg cac atc gaa ggt gcc ttg gaa tat gga atc aca agt gat	627
Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp	
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gac atc ttc tgg ctg aag gaa tcc cct gga aaa acg ttg gtg gtc ggg	675
Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly	
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Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly	
225 230 235	
ctg gac acc acc atc atg atg cgc agc atc ccc ctc cgc ggc ttc gac	771
Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp	
240 245 250	
cag caa atg tcc tcc atg gtc ata gag cac atg gca tct cat ggc acc	819
Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr	
255 260 265 270	
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Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp	
275 280 285	
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Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp	
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 Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp
 305 310 315

acc aga agt ctg aat ttg gag aag gct ggg gta gat act agc ccc gac 1011
 Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp
 320 325 330

act cag aag atc ctg gtg gac tcc cgg gaa gcc acc tct gtg ccc cac 1059
 Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His
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atc tac gcc att ggt gac gtg gtg gag ggg cgg cct gag ctg aca ccc 1107
 Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro
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aca gcg atc atg gcc ggg agg ctc ctg gtg cag cgg ctc ttc ggc ggg 1155
 Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly
 370 375 380

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 Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr
 385 390 395

cca ctg gag tat ggc tgt gtg ggg ctg tcc gag gag gag gca gtg gct 1251
 Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala
 400 405 410

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 Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro
 415 420 425 430

ctg gag ttc acg gtg gct gga cga gat gca tcc cag tgt tat gta aag 1347
 Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys
 435 440 445

atg gtg tgc ctg agg gag ccc cca cag ctg gtg ctg ggc ctg cat ttc 1395
 Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe
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ctt ggc ccc aac gca ggc gaa gtt act caa gga ttt gct ctg ggg atc 1443
 Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile
 465 470 475

aag tgt ggg gct tcc tat gcg cag gtg atg cgg acc gtg ggt atc cat 1491
 Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His
 480 485 490

ccc aca tgc tct gag gag gta gtc aag ctg cgc atc tcc aag cgc tca 1539
 Pro Thr Cys Ser Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser
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 Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
 515 520

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 <223> Selenocysteine

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 35 40 45
 Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val Ala Val
 50 55 60
 Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly Leu Gly
 65 70 75 80
 Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln
 85 90 95
 Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr Gly Trp
 100 105 110
 Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala Glu Ala
 115 120 125
 Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val Gln Leu
 130 135 140
 Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe Val Asp
 145 150 155 160
 Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile Leu Leu
 165 170 175

Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg Tyr Pro
 180 185 190
 Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp Asp Ile
 195 200 205
 Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly Ala Ser
 210 215 220
 Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly Leu Asp
 225 230 235 240
 Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp Gln Gln
 245 250 255
 Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr Arg Phe
 260 265 270
 Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp Gly Gln
 275 280 285
 Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp Thr Gly
 290 295 300
 Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp Thr Arg
 305 310 315 320
 Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp Thr Gln
 325 330 335
 Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His Ile Tyr
 340 345 350
 Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro Thr Ala
 355 360 365
 Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly Ser Ser
 370 375 380
 Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr Pro Leu
 385 390 395 400
 Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala Arg His
 405 410 415
 Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro Leu Glu
 420 425 430
 Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys Met Val
 435 440 445
 Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe Leu Gly
 450 455 460
 Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile Lys Cys
 465 470 475 480

Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His Pro Thr
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<222> (188)..(1669)

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agtagacacg atgacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg 180

agccacc atg gag gac caa gca ggt cag cgg gac tat gat ctc ctg gtg 229
 Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val
 1 5 10

gtc ggc ggg gga tct ggt ggc ctg gct tgt gcc aag gag gcc gcc cag 277
 Val Gly Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln
 15 20 25 30

ctg gga agg aag gtg gcc gtg gtg gac tac gtg gaa cct tct ccc caa 325
 Leu Gly Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln
 35 40 45

ggc acc cgg tgg ggc ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc 373
 Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile
 50 55 60

ccc aag aag ctg atg cac cag gcg gca ctg ctg gga ggc ctg atc caa 421
 Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln
 65 70 75

gat gcc ccc aac tat ggc tgg gag gtg gcc cag ccc gtg ccg cat gac 469
 Asp Ala Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp
 80 85 90

tgg agg aag atg gca gaa gct gtt caa aat cac gtg aaa tcc ttg aac 517
 Trp Arg Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn
 95 100 105 110

tgg ggc cac cgt gtc cag ctt cag gac aga aaa gtc aag tac ttt aac	565
Trp Gly His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn	
115 120 125	
atc aaa gcc agc ttt gtt gac gag cac acg gtt tgc ggc gtt gcc aaa	613
Ile Lys Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys	
130 135 140	
ggt ggg aaa gag att ctg ctg tca gcc gat cac atc atc att gct act	661
Gly Gly Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr	
145 150 155	
gga ggg cgg ccg aga tac ccc acg cac atc gaa ggt gcc ttg gaa tat	709
Gly Gly Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr	
160 165 170	
gga atc aca agt gat gac atc ttc tgg ctg aag gaa tcc cct gga aaa	757
Gly Ile Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys	
175 180 185 190	
acg ttg gtg gtc ggg gcc agc tat gtg gcc ctg gag tgt gct ggc ttc	805
Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe	
195 200 205	
ctc acc ggg att ggg ctg gac acc acc atc atg atg cgc agc atc ccc	853
Leu Thr Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro	
210 215 220	
ctc cgc ggc ttc gac cag caa atg tcc tcc atg gtc ata gag cac atg	901
Leu Arg Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met	
225 230 235	
gca tct cat ggc acc cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc	949
Ala Ser His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val	
240 245 250	
agg agg ctc cct gat ggc cag ctg cag gtc acc tgg gag gac agc acc	997
Arg Arg Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr	
255 260 265 270	
acc ggc aag gag gac acg ggc acc ttt gac acc gtc ctg tgg gcc ata	1045
Thr Gly Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile	
275 280 285	
ggt cga gtc cca gac acc aga agt ctg aat ttg gag aag gct ggg gta	1093
Gly Arg Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val	
290 295 300	
gat act agc ccc gac act cag aag atc ctg gtg gac tcc cgg gaa gcc	1141
Asp Thr Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala	
305 310 315	
acc tct gtg ccc cac atc tac gcc att ggt gac gtg gtg gag ggg cgg	1189
Thr Ser Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg	
320 325 330	

cct gag ctg aca ccc aca gcg atc atg gcc ggg agg ctc ctg gtg cag	1237
Pro Glu Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln	
335 340 345 350	
egg ctc ttc ggc ggg tcc tca gat ctg atg gac tac gac aat gtt ccc	1285
Arg Leu Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro	
355 360 365	
acg acc gtc ttc acc cca ctg gag tat ggc tgt gtg ggg ctg tcc gag	1333
Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu	
370 375 380	
gag gag gca gtg gct cgc cac ggg cag gag cat gtt gag gtc tat cac	1381
Glu Glu Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His	
385 390 395	
gcc cat tat aaa cca ctg gag ttc acg gtg gct gga cga gat gca tcc	1429
Ala His Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser	
400 405 410	
cag tgt tat gta aag atg gtg tgc ctg agg gag ccc cca cag ctg gtg	1477
Gln Cys Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val	
415 420 425 430	
ctg ggc ctg cat ttc ctt ggc ccc aac gca ggc gaa gtt act caa gga	1525
Leu Gly Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly	
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Phe Ala Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg	
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acc gtg ggt atc cat ccc aca tgc tct gag gag gta gtc aag ctg cgc	1621
Thr Val Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg	
465 470 475	
atc tcc aag cgc tca ggc ctg gac ccc acg gtg aca ggc tgc tga ggg	1669
Ile Ser Lys Arg Ser Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly	
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agaccagga tggctgcagg ccagggtttgg ggggectcaa ccctctcctg gagcgccctgt	1789
gagatgggtca gcgtggagcg caagtgtctgg acgggtggcc cgtgtgcccc acaggggatgg	1849
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<213> Homo sapiens

<220>

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<222> (493)

<223> Selenocysteine

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Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr
 35 40 45

Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys
 50 55 60

Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala
 65 70 75 80

Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg
 85 90 95

Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly
 100 105 110

His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys
 115 120 125

Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly
 130 135 140

Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly
 145 150 155 160

Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile
 165 170 175

Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu
 180 185 190

Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr
 195 200 205

Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg
 210 215 220

Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser
 225 230 235 240

His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg
 245 250 255

Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly
 260 265 270
 Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg
 275 280 285
 Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr
 290 295 300
 Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser
 305 310 315 320
 Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu
 325 330 335
 Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu
 340 345 350
 Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr
 355 360 365
 Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu
 370 375 380
 Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His
 385 390 395 400
 Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys
 405 410 415
 Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly
 420 425 430
 Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala
 435 440 445
 Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val
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<212> DNA

<213> Homo sapiens

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<210> 7
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<220>
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<400> 9
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<210> 10
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<212> DNA
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<400> 10
 acagcttctg ccattcttct c 21

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<210> 12
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 ccaaggagg 69

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 tggcccagcc cgtgccgcat gactg 145

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 ccagcttcag gacag 75

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 <212> DNA
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<223> Description of Unknown Organism: Thioredoxin
 reductase

<220>

<221> MOD_RES

<222> (498)

<223> Selenocysteine

<400> 38

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Gln	Tyr	Gly	Lys	Lys	Val	Met	Val	Leu	Asp	Phe	Val	Thr	Pro	Thr	Pro	35	40	45	
Leu	Gly	Thr	Arg	Trp	Gly	Leu	Gly	Gly	Thr	Cys	Val	Asn	Val	Gly	Cys	50	55	60	
Ile	Pro	Lys	Lys	Leu	Met	His	Gln	Ala	Ala	Leu	Leu	Gly	Gln	Ala	Leu	65	70	75	80
Gln	Asp	Ser	Arg	Asn	Tyr	Gly	Trp	Lys	Val	Glu	Glu	Tyr	Val	Lys	His	85	90	95	
Asp	Trp	Asp	Arg	Met	Ile	Glu	Ala	Val	Gln	Asn	His	Ile	Gly	Ser	Leu	100	105	110	
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Asn	Lys	Gly	Lys	Glu	Lys	Ile	Tyr	Ser	Ala	Glu	Ser	Phe	Leu	Ile	Ala	145	150	155	160
Thr	Gly	Glu	Arg	Pro	Arg	Tyr	Leu	Gly	Ile	Pro	Gly	Asp	Lys	Glu	Tyr	165	170	175	
Cys	Ile	Ser	Ser	Asp	Asp	Leu	Phe	Ser	Leu	Pro	Tyr	Cys	Pro	Gly	Lys	180	185	190	
Thr	Leu	Val	Val	Gly	Ala	Ser	Tyr	Val	Ala	Leu	Glu	Cys	Ala	Gly	Phe	195	200	205	
Leu	Ala	Gly	Ile	Gly	Leu	Gly	Val	Thr	Val	Met	Val	Arg	Ser	Ile	Leu	210	215	220	
Leu	Arg	Gly	Phe	Asp	Gln	Asp	Met	Ala	Asn	Lys	Ile	Gly	Glu	His	Met	225	230	235	240

Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val Pro Ile Lys Val
245 250 255

Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg Val Val Ala Gln
260 265 270

Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr Asn Thr Val Met
275 280 285

Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile Gly Leu Glu Thr
290 295 300

Val	Gly	Val	Lys	Ile	Asn	Glu	Lys	Thr	Gly	Lys	Ile	Pro	Val	Thr	Asp
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Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile Gly Asp Ile Leu
325 330 335

Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln Ala Gly Arg Leu
340 345 350

Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys Cys Asp Tyr Glu
355 360 365

Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Ala Cys Gly
370 375 380

Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu Glu Asn Ile Glu
385 390 395 400

Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr Ile Pro Ser Arg
405 410 415

Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn Thr Lys Asp Asn
420 425 430

Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn Ala Gly Glu Val
435 440 445

Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu Thr Lys Lys Gln
450 455 460

Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala Glu Val Phe Thr
465 470 475 480

Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser Ile Leu Gln Ala Gly
485 490 495

Cys Xaa Gly